FASTA searches a protein or DNA sequence data bank
 version 3.3t05 March 30, 2000
Please cite:
 W.R. Pearson & D.J. Lipman PNAS (1988) 85:2444-2448

/tmp/fastaCAAUTa4Xs: 1214 aa
 >seqid4
 vs   /tmp/fastaDAAVTa4Xs library
searching /tmp/fastaDAAVTa4Xs library

   1258 residues in   1 sequences

FASTA (3.34 January 2000) function [optimized, BL50 matrix (15:-5)] ktup: 2
 join: 40, opt: 28, gap-pen: -12/ -2, width: 16
 Scan time: 0.034
The best scores are: opt
sp|Q96PY6|NEK1_HUMAN Serine/threonine-protein kin   (1258) 4775

>>sp|Q96PY6|NEK1_HUMAN Serine/threonine-protein kinase N (1258 aa)
 initn: 4773 init1: 4773 opt: 4775
Smith-Waterman score: 7822; 96.343% identity in 1258 aa overlap (1-1214:1-1258)

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              10        20        30        40        50        60
seqid4 MEKYVRLQKIGEGSFGKAILVKSTEDGRQYVIKEINISRMSSKEREESRREVAVLANMKH
       :::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
sp|Q96 MEKYVRLQKIGEGSFGKAILVKSTEDGRQYVIKEINISRMSSKEREESRREVAVLANMKH
              10        20        30        40        50        60


              70        80        90       100       110       120
seqid4 PNIVQYRESFEENGSLYIVMDYCEGGDLFKRINAQKGVLFQEDQILDWFVQICLALKHVH
       :::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
sp|Q96 PNIVQYRESFEENGSLYIVMDYCEGGDLFKRINAQKGVLFQEDQILDWFVQICLALKHVH
              70        80        90       100       110       120


             130       140       150       160       170       180
seqid4 DRKILHRDIKSQNIFLTKDGTVQLGDFGIARVLNSTVELARTCIGTPYYLSPEICENKPY
       :::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
sp|Q96 DRKILHRDIKSQNIFLTKDGTVQLGDFGIARVLNSTVELARTCIGTPYYLSPEICENKPY
             130       140       150       160       170       180


             190       200       210       220       230       240
seqid4 NNKSDIWALGCVLYELCTLKHAFEAGSMKNLVLKIISGSFPPVSLHYSYDLRSLVSQLFK
       :::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
sp|Q96 NNKSDIWALGCVLYELCTLKHAFEAGSMKNLVLKIISGSFPPVSLHYSYDLRSLVSQLFK
             190       200       210       220       230       240


             250       260       270       280       290       300
seqid4 RNPRDRPSVNSILEKGFIAKRIEKFLSPQLIAEEFCLKTFSKFGSQPIPAKRPASGQNSI
       :::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
sp|Q96 RNPRDRPSVNSILEKGFIAKRIEKFLSPQLIAEEFCLKTFSKFGSQPIPAKRPASGQNSI
             250       260       270       280       290       300


             310       320       330       340       350       360
seqid4 SVMPAQKITKPAAKYGIPLAYKKYGDKKLHEKKPLQKHKQAHQTPEKRVNTGEERRKISE
       :::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
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sp|Q96  SVMPAQKITKPAAKYGIPLAYKKYGDKKLHEKKPLQKHKQAHQTPEKRVNTGEERRKISE
                310       320       330       340       350       360


                370       380       390       400       410       420
seqid4  EAARKRRLEFIEKEKKQKDQIISLMKAEQMKRQEKERLERINRAREQGWRNVLSAGGSGE
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
sp|Q96  EAARKRRLEFIEKEKKQKDQIISLMKAEQMKRQEKERLERINRAREQGWRNVLSAGGSGE
                370       380       390       400       410       420


                430       440       450       460       470
seqid4  VKAPFLGSGGTIAPSSFSSRGQYEHYHAIFDQMQQQRAEDNEAKWKREIYGRGLPER---
        :::::::::::::::::::::::::::::::::::::::::::::::::::::::::
sp|Q96  VKAPFLGSGGTIAPSSFSSRGQYEHYHAIFDQMQQQRAEDNEAKWKREIYGRGLPERGIL
                430       440       450       460       470       480


                                                    480       490
seqid4  ------------------------------------------QKGQLAVERAKQVEEFLQR
                                                  :::::::::::::::::::
sp|Q96  PGVRPGFPYGAAGHHHFPDADDIRKTLKRLKAVSKQANANRQKGQLAVERAKQVEEFLQR
                490       500       510       520       530       540


                500       510       520       530       540       550
seqid4  KREAMQNKARAEGHMVYLARLRQIRLQNFNERQQIKAKLRGEKKEANHSEGQEGSEEADM
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
sp|Q96  KREAMQNKARAEGHMVYLARLRQIRLQNFNERQQIKAKLRGEKKEANHSEGQEGSEEADM
                550       560       570       580       590       600


                560       570       580       590       600       610
seqid4  RRKKIESLKAHANARAAVLKEQLERKRKEAYEREKKVWEEHLVAKGVKSSDVSPPLGQHE
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
sp|Q96  RRKKIESLKAHANARAAVLKEQLERKRKEAYEREKKVWEEHLVAKGVKSSDVSPPLGQHE
                610       620       630       640       650       660


                620       630       640       650       660       670
seqid4  TGGSPSKQQMRSVISVTSALKEVGVDSSLTDTRETSEEMQKTNNAISSKREILRRLNENL
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
sp|Q96  TGGSPSKQQMRSVISVTSALKEVGVDSSLTDTRETSEEMQKTNNAISSKREILRRLNENL
                670       680       690       700       710       720


                680       690       700       710       720       730
seqid4  KAQEDEKGMQNLSDTFEINVHEDAKEHEKEKSVSSDRKKWEAGGQLVIPLDELTLDTSFS
        ::::::::  ::::::::::::::::::::::::::::::::::::::::::::::::::::
sp|Q96  KAQEDEKGKQNLSDTFEINVHEDAKEHEKEKSVSSDRKKWEAGGQLVIPLDELTLDTSFS
                730       740       750       760       770       780


                740       750       760       770       780       790
seqid4  TTERHTVGEVIKLGPNGSPRRAWGKSPTDSVLKILGEAELQLQTELLENTTIRSEISPEG
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
sp|Q96  TTERHTVGEVIKLGPNGSPRRAWGKSPTDSVLKILGEAELQLQTELLENTTIRSEISPEG
                790       800       810       820       830       840


                800       810       820       830       840       850
seqid4  EKYKPLITGEKKVQCISHEINPSAIVDSPVETKSPEFSEASPQMSLKLEGNLEEPDDLET
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
sp|Q96  EKYKPLITGEKKVQCISHEINPSAIVDSPVETKSPEFSEASPQMSLKLEGNLEEPDDLET
                850       860       870       880       890       900


                860       870       880       890       900       910
seqid4  EILQEPSGTNKDESLPCTITDVWISEEKETKETQSADRITIQENEVSEDGVSSTVDQLSD
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
sp|Q96  EILQEPSGTNKDESLPCTITDVWISEEKETKETQSADRITIQENEVSEDGVSSTVDQLSD
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                910        920        930        940        950        960

           920        930        940        950        960        970
seqid4  IHIEPGTNDSQHSKCDVDKSVQPEPFFHKVVHSEHLNLVPQVQSVQCSPEESFAFRSHSH
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
sp|Q96  IHIEPGTNDSQHSKCDVDKSVQPEPFFHKVVHSEHLNLVPQVQSVQCSPEESFAFRSHSH
               970        980        990        1000       1010       1020


           980        990        1000       1010       1020       1030
seqid4  LPPKNKNKNSLLIGLSTGLFDANNPKMLRTCSLPDLSKLFRTLMDVPTVGDVRQDNLEID
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
sp|Q96  LPPKNKNKNSLLIGLSTGLFDANNPKMLRTCSLPDLSKLFRTLMDVPTVGDVRQDNLEID
               1030       1040       1050       1060       1070       1080


           1040       1050       1060       1070       1080       1090
seqid4  EIKDENIKEGPSDSEDIVFEETDTDLQELQASMEQLLREQPGEEYSEEEESVLKNSDVEP
        ::.::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
sp|Q96  EIEDENIKEGPSDSEDIVFEETDTDLQELQASMEQLLREQPGEEYSEEEESVLKNSDVEP
               1090       1100       1110       1120       1130       1140


           1100       1110       1120       1130       1140       1150
seqid4  TANGTDVADEDDNPSSESALNEEWHSDNSDGEIASECECDSVFNHLEELRLHLEQEMGFE
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
sp|Q96  TANGTDVADEDDNPSSESALNEEWHSDNSDGEIASECECDSVFNHLEELRLHLEQEMGFE
               1150       1160       1170       1180       1190       1200


           1160       1170       1180       1190       1200       1210
seqid4  KFFEVYEKIKAIHEDEDENIEICSKIVQNILGNEHQHLYAKILHLVMADGAYQEDNDE
        :::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
sp|Q96  KFFEVYEKIKAIHEDEDENIEICSKIVQNILGNEHQHLYAKILHLVMADGAYQEDNDE
               1210       1220       1230       1240       1250
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